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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/884,566A

DATE: 02/14/2002
 TIME: 09:27:02

Input Set : A:\37497.txt
 Output Set: N:\CRF3\02142002\I884566A.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: Keegan, Kathleen S.
- 8 (ii) TITLE OF INVENTION: Novel CREBa Isoform
- 10 (iii) NUMBER OF SEQUENCES: 10
- 12 (iv) CORRESPONDENCE ADDRESS:
 - 13 (A) ADDRESSEE: Marshall, Gerstein & Borun
 - 14 (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
 - 15 (C) CITY: Chicago
 - 16 (D) STATE: Illinois
 - 17 (E) COUNTRY: USA
 - 18 (F) ZIP: 60606

20 (v) COMPUTER READABLE FORM:

- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

- C--> 27 (A) APPLICATION NUMBER: US/09/884,566A
- C--> 28 (B) FILING DATE: 19-Jun-2001
- 29 (C) CLASSIFICATION:

31 (viii) ATTORNEY/AGENT INFORMATION:

- 32 (A) NAME: Williams Jr., Joseph A.
- 33 (B) REGISTRATION NUMBER: 38,659
- 34 (C) REFERENCE/DOCKET NUMBER: 27866/37497

36 (ix) TELECOMMUNICATION INFORMATION:

- 37 (A) TELEPHONE: 312-474-6300
- 38 (B) TELEFAX: 312-474-0448

41 (2) INFORMATION FOR SEQ ID NO: 1:

- 43 (i) SEQUENCE CHARACTERISTICS:
 - 44 (A) LENGTH: 3190 base pairs
 - 45 (B) TYPE: nucleic acid
 - 46 (C) STRANDEDNESS: single
 - 47 (D) TOPOLOGY: linear

49 (ii) MOLECULE TYPE: cDNA

- 52 (ix) FEATURE:
 - 53 (A) NAME/KEY: CDS
 - 54 (B) LOCATION: 304..1866

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTGG CTTCCCTTTG GATGCACAGC	60
61 CCGATTTAAC CCCTGCACCT TCCGCCGAT CCCAGCAGGC TTGTCCCTCCC CGGGGAGTC	120
63 CAGATTTCCG AGGACAAGGG TCGCGTAGCC TTCGGCAGGG CTCTCCCGAG TTCCTGCTCC	180
65 AGTGCATAAG TTCCACCGCGC GCACACGCCA AGTACACGGG GAGAAGCGTC TCACCGGCC	240

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67	GCGGCGGCTC	TGCGCGGTCC	CCTCCTGCCT	CAGCATCCTC	GGGCCTGCGC	GGCGCCCACC	300											
69	GCC	ATG	GAG	GTG	CTG	GAG	AGC	GGG	GAG	CAG	AGC	GTC	CTG	CAG	TGG	GAC	348	
70	Met	Glu	Val	Leu	Glu	Ser	Gly	Glu	Gln	Ser	Val	Leu	Gln	Trp	Asp			
71	1			5				10				15						
73	CGC	AAG	CTG	AGC	GAG	CTG	TCA	GAG	CCC	GGA	GAG	ACT	GAG	GCC	CTC	ATG	396	
74	Arg	Lys	Leu	Ser	Glu	Leu	Ser	Glu	Pro	Gly	Glu	Thr	Glu	Ala	Leu	Met		
75				20				25				30						
77	TAC	CAC	ACG	CAC	TTC	TCG	GAG	CTC	CTA	GAC	GAG	TTT	TCC	CAG	AAC	GTC	444	
78	Tyr	His	Thr	His	Phe	Ser	Glu	Leu	Leu	Asp	Glu	Phe	Ser	Gln	Asn	Val		
79				35				40				45						
81	CTG	GGT	CAG	CTC	CTG	AGT	GAC	CCT	TTC	CTC	TCA	GAG	AAG	AGC	GAG	TCA	492	
82	Leu	Gly	Gln	Leu	Leu	Ser	Asp	Pro	Phe	Leu	Ser	Glu	Lys	Ser	Glu	Ser		
83				50				55				60						
85	ATG	GAG	GTG	GAG	CCA	TCT	CCA	ACA	TCA	CCA	GCG	CCT	CTC	ATC	CAG	GCT	540	
86	Met	Glu	Val	Glu	Pro	Ser	Pro	Thr	Ser	Pro	Ala	Pro	Leu	Ile	Gln	Ala		
87				65				70				75						
89	GAA	CAC	AGC	TAC	TCT	CTG	AGC	GAG	GAG	CCC	CGG	ACT	CAG	TCA	CCA	TTT	588	
90	Glu	His	Ser	Tyr	Ser	Leu	Ser	Glu	Glu	Pro	Arg	Thr	Gln	Ser	Pro	Phe		
91				80				85				90				95		
93	ACC	CAT	GCG	GCT	ACC	AGC	GAC	AGC	TTC	AAT	GAC	GAG	GAG	GTG	GAG	AGT	636	
94	Thr	His	Ala	Ala	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Glu	Glu	Val	Glu	Ser		
95					100				105				110					
97	GAA	AAA	TGG	TAC	CTG	TCT	ACA	GAG	TTT	CCT	TCA	GCT	ACC	ATC	AAG	AAA	684	
98	Glu	Lys	Trp	Tyr	Leu	Ser	Thr	Glu	Phe	Pro	Ser	Ala	Thr	Ile	Lys	Lys		
99					115				120				125					
101	GAG	CCA	ATC	ACA	GAG	GAG	CAG	CCC	CCG	GGA	CTT	GTC	CCT	TCT	GTC	ACT	732	
102	Glu	Pro	Ile	Thr	Glu	Glu	Gln	Pro	Pro	Gly	Leu	Val	Pro	Ser	Val	Thr		
103				130				135				140						
105	CTG	ACC	ATC	ACA	GCC	ATT	TCC	ACT	CCT	TTT	GAA	AAA	GAA	GAG	TCC	CCT	780	
106	Leu	Thr	Ile	Thr	Ala	Ile	Ser	Thr	Pro	Phe	Glu	Lys	Glu	Glu	Ser	Pro		
107				145				150				155						
109	CTG	GAT	ATG	AAT	GCT	GGG	GGG	GAC	TCC	TCA	TGC	CAG	ACG	CTT	ATT	CCT	828	
110	Leu	Asp	Met	Asn	Ala	Gly	Gly	Asp	Ser	Ser	Cys	Gln	Thr	Leu	Ile	Pro		
111				160				165				170				175		
113	AAG	ATT	AAG	CTG	GAG	CCC	CAC	GAA	GTG	GAT	CAG	TTC	TTA	AAC	TTC	TCC	876	
114	Lys	Ile	Lys	Leu	Glu	Pro	His	Glu	Val	Asp	Gln	Phe	Leu	Asn	Phe	Ser		
115					180				185				190					
117	CCG	AAA	GAA	GCC	TCC	GTG	GAT	CAA	CTG	CAC	TTA	CCA	CCA	ACA	CCA	CCC	924	
118	Pro	Lys	Glu	Ala	Ser	Val	Asp	Gln	Leu	His	Leu	Pro	Pro	Thr	Pro	Pro		
119				195				200				205						
121	AGT	AGT	CAC	AGC	AGT	GAC	TCT	GAG	GGC	AGC	TTG	AGC	CCC	AAC	CCA	CGC	972	
122	Ser	Ser	His	Ser	Ser	Asp	Ser	Glu	Gly	Ser	Leu	Ser	Pro	Asn	Pro	Arg		
123				210				215				220						
125	CTG	CAT	CCC	TTC	AGC	CTG	TCT	CAG	GCC	CAC	AGC	CCT	GTC	AGA	GCC	ATG	1020	
126	Leu	His	Pro	Phe	Ser	Leu	Ser	Gln	Ala	His	Ser	Pro	Val	Arg	Ala	Met		
127				225				230				235						
129	CCC	CGG	GGC	CCC	TCT	GCC	TTG	TCC	ACA	TCT	CCT	CTC	CTC	ACA	GCT	CCA	1068	
130	Pro	Arg	Gly	Pro	Ser	Ala	Leu	Ser	Thr	Ser	Pro	Leu	Leu	Thr	Ala	Pro		
131				240				245				250				255		

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133	CAT	AAG	CTG	CAG	GGA	TCG	GGC	CCC	CTG	GTC	CTG	ACA	GAA	GAG	GAG	AAG	1116
134	His	Lys	Leu	Gln	Gly	Ser	Gly	Pro	Leu	Val	Leu	Thr	Glu	Glu	Glu	Lys	
135				260					265				270				
137	AGG	ACC	CTG	GTT	GCC	GAG	GGC	TAT	CCC	ATT	CCC	ACC	AAG	CTG	CCT	CTG	1164
138	Arg	Thr	Leu	Val	Ala	Glu	Gly	Tyr	Pro	Ile	Pro	Thr	Lys	Leu	Pro	Leu	
139					275				280				285				
141	ACA	AAA	TCT	GAG	GAG	AAG	GCC	CTG	AAG	AAA	ATC	CGG	AGA	AAG	ATC	AAG	1212
142	Thr	Lys	Ser	Glu	Glu	Lys	Ala	Leu	Lys	Lys	Ile	Arg	Arg	Lys	Ile	Lys	
143				290				295			300						
145	AAT	AAG	ATT	TCT	GCC	CAA	GAA	AGC	AGG	AGA	AAG	AAG	AAA	GAA	TAC	ATG	1260
146	Asn	Lys	Ile	Ser	Ala	Gln	Glu	Ser	Arg	Arg	Lys	Lys	Lys	Glu	Tyr	Met	
147				305				310			315						
149	GAC	AGC	CTG	GAG	AAA	AAA	GTG	GAG	TCT	TGT	TCA	ACT	GAG	AAC	TTG	GAG	1308
150	Asp	Ser	Leu	Glu	Lys	Lys	Val	Glu	Ser	Cys	Ser	Thr	Glu	Asn	Leu	Glu	
151	320				325				330			335					
153	CTT	CGG	AAG	AAG	GTG	GAG	GTG	CTG	GAG	AAC	ACC	AAT	AGG	ACT	CTC	CTT	1356
154	Leu	Arg	Lys	Lys	Val	Glu	Val	Leu	Glu	Asn	Thr	Asn	Arg	Thr	Leu	Leu	
155					340				345			350					
157	CAG	CAA	CTT	CAG	AAG	CTT	CAG	ACT	TTG	GTG	ATG	GGG	AAG	GTC	TCT	CGA	1404
158	Gln	Gln	Leu	Gln	Lys	Leu	Gln	Thr	Leu	Val	Met	Gly	Lys	Val	Ser	Arg	
159				355				360			365						
161	ACC	TGC	AAG	TTA	GCT	GGC	ACA	CAG	ACT	GGC	ACC	TGC	CTC	ATG	GTC	GTT	1452
162	Thr	Cys	Lys	Leu	Ala	Gly	Thr	Gln	Thr	Gly	Thr	Cys	Leu	Met	Val	Val	
163				370				375			380						
165	GTG	CTT	TGC	TTT	GCT	GTT	GCA	TTT	GGA	AGC	TTC	TTT	CAA	GGC	TAT	GGG	1500
166	Val	Leu	Cys	Phe	Ala	Val	Ala	Phe	Gly	Ser	Phe	Phe	Gln	Gly	Tyr	Gly	
167				385				390			395						
169	CCT	TAT	CCT	TCT	GCC	ACC	AAG	ATG	GCT	CTG	CCC	AGC	CAG	CAT	CCT	CTG	1548
170	Pro	Tyr	Pro	Ser	Ala	Thr	Lys	Met	Ala	Leu	Pro	Ser	Gln	His	Pro	Leu	
171	400				405				410			415					
173	TCA	GAG	CCA	TAC	ACA	GCC	TCC	GTG	GTG	AGA	TCC	AGG	AAC	CTG	CTA	ATC	1596
174	Ser	Glu	Pro	Tyr	Thr	Ala	Ser	Val	Val	Arg	Ser	Arg	Asn	Leu	Ile		
175					420				425			430					
177	TAT	GAG	GAA	CAC	GCT	CCC	CTG	GAA	GAG	TCG	TCG	AGC	CCA	GCC	TCA	ACC	1644
178	Tyr	Glu	Glu	His	Ala	Pro	Leu	Glu	Glu	Ser	Ser	Ser	Pro	Ala	Ser	Thr	
179				435				440			445						
181	GGG	GAG	CTG	GGG	GGC	TGG	GAC	AGA	GGC	TCC	TCT	CTG	CTC	AGG	GCA	TCG	1692
182	Gly	Glu	Leu	Gly	Gly	Trp	Asp	Arg	Gly	Ser	Ser	Leu	Leu	Arg	Ala	Ser	
183				450				455			460						
185	TCG	GGG	CTT	GAG	GCC	CTG	CCA	GAG	GTG	GAT	CTT	CCC	CAT	TTC	CTT	ATC	1740
186	Ser	Gly	Leu	Glu	Ala	Leu	Pro	Glu	Val	Asp	Leu	Pro	His	Phe	Leu	Ile	
187					465			470			475						
189	TCC	AAT	GAG	ACG	AGC	TTG	GAG	AAG	TCA	GTA	CTG	TTG	GAG	CTT	CAG	CAG	1788
190	Ser	Asn	Glu	Thr	Ser	Leu	Glu	Lys	Ser	Val	Leu	Leu	Glu	Leu	Gln	Gln	
191	480				485				490			495					
193	CAC	CTG	GTC	AGC	AGC	AAA	CTG	GAA	GGG	AAC	GAA	ACA	CTC	AAG	GTT	GTA	1836
194	His	Leu	Val	Ser	Ser	Lys	Leu	Glu	Gly	Asn	Glu	Thr	Leu	Lys	Val	Val	
195					500				505			510					
197	GAG	CTG	GAG	AGG	AGA	GTG	AAC	GCC	ACC	TTC	TGAGGAGAGC	TCCACCTCC					1886

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198 Glu Leu Glu Arg Arg Val Asn Ala Thr Phe
 199 515 520

201 TCTTCTCCTA ACTCCATCTG ATCGTCCTT CAGTTCCCC TTCACCACTG GATCTCGAGG 1946
 203 AGGAGATGGC TAGTGTACG GCTCGAGACA GGAGGCCAGC CCAGGGGTT CTGCTTATGT 2006
 205 GTCCCCGTGG CTCTCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTCT CTTACTGCCA 2066
 207 TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTT CCACCAATAG 2126
 209 TGCCAAGAAC ACACGCCTG ATTCTTCCC GGGAGGAGTG ACTCCTCTGA AGAAGACATG 2186
 211 ACTCATGTTC AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA 2246
 213 GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCCTGCAC 2306
 215 TGAGAGGACC AAAGCGTCAT TGCAGTCTC TCTCCACCT GTACCCGGGA GTCTGATTG 2366
 217 GATGTCTGCA GAGGCAGATG GGGCTCCAC CATATTTCA GGCGCAAGT GCAATTCTG 2426
 219 AAGGCATCAG GCTCTCTCT CCCAGGCTCT CCTGCCACT GTGTTGTTG TAGGACACCC 2486
 221 CCACACCCAC TCATAACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT 2546
 223 CCCCTCCCCA TTTGTAATAA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG 2606
 225 AAAAGATTTT CCCTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGGAAACA GGAGAGTCCC 2666
 227 CGGAATCTAG GACCCCTAGTC TTTGTACTTG ATGCCTGTT TCCCCCCTTT TCTCTTTAA 2726
 229 AATTGGGGAC CTATAACATC ATCGCTGTG CGGAATCCAC TTAGGCATGT GTCCCTGTAT 2786
 231 GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT 2846
 233 TCTCTCTCT GGTCCCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG 2906
 235 ACACCCCTTG TAGCTTGTCC TGCCTACCTG CTTACCCAC TCCCTCACCT TCCTCCTTCC 2966
 237 CTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTGTAC 3026
 239 ACCCACAGTG GTACCTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA 3086
 241 TAACTAAACC CTAAACTCTT TTTTGTGTT TGTTGTTGTT GTTTTTTTT TTTATGATTA 3146
 243 AAAAGTAAAA ATTGTAGTTT AAAAAAAAAA AAAAAAAACT CGAG 3190

246 (2) INFORMATION FOR SEQ ID NO: 2:

248 (i) SEQUENCE CHARACTERISTICS:

249 (A) LENGTH: 521 amino acids
 250 (B) TYPE: amino acid
 251 (D) TOPOLOGY: linear

253 (ii) MOLECULE TYPE: protein

255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

257 Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg
 258 1 5 10 15
 260 Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr
 261 20 25 30
 263 His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
 264 35 40 45
 266 Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met
 267 50 55 60
 269 Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
 270 65 70 75 80
 272 His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr
 273 85 90 95
 275 His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu
 276 100 105 110
 278 Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu
 279 115 120 125
 281 Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu
 282 130 135 140

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284 Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu
 285 145 150 155 160
 287 Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys
 288 165 170 175
 290 Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro
 291 180 185 190
 293 Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser
 294 195 200 205
 296 Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu
 297 210 215 220
 299 His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro
 300 225 230 235 240
 302 Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His
 303 245 250 255
 305 Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Lys Arg
 306 260 265 270
 308 Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr
 309 275 280 285
 311 Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn
 312 290 295 300
 314 Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp
 315 305 310 315 320
 317 Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu
 318 325 330 335
 320 Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln
 321 340 345 350
 323 Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr
 324 355 360 365
 326 Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val
 327 370 375 380
 329 Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro
 330 385 390 395 400
 332 Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser
 333 405 410 415
 335 Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr
 336 420 425 430
 338 Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly
 339 435 440 445
 341 Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser
 342 450 455 460
 344 Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser
 345 465 470 475 480
 347 Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His
 348 485 490 495
 350 Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu
 351 500 505 510
 353 Leu Glu Arg Arg Val Asn Ala Thr Phe
 354 515 520
 356 (2) INFORMATION FOR SEQ ID NO: 3:

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/884,566A

DATE: 02/14/2002

TIME: 09:27:03

Input Set : A:\37497.txt

Output Set: N:\CRF3\02142002\I884566A.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:426 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]